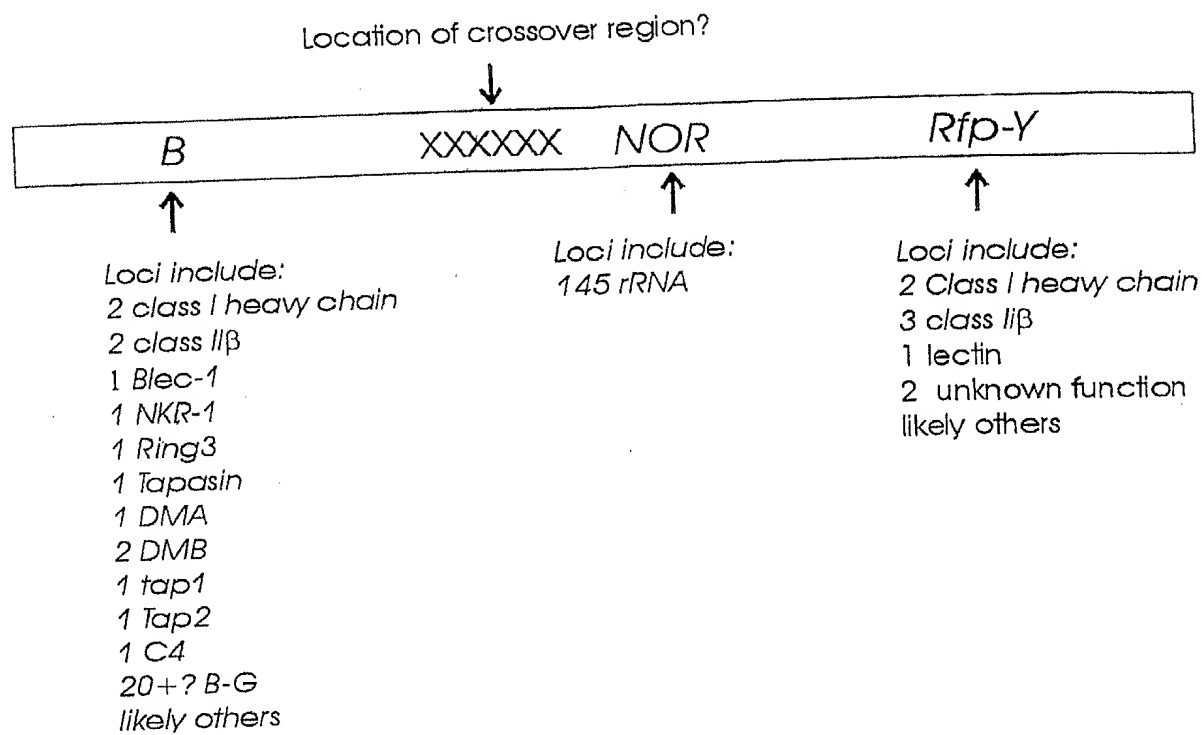


Figure 1



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[illegible]

Figure 2B

<< 178/179f(bold)>>

Figure 3

<i>a1 domain</i>	10.	20.	30.	40.	50.	60.	70.	80.
YFV <sub>w</sub> *7	GSHSLRYFLTGMDPGPGMPRFVIVGVDDKIFGTYNKSRTAQPIVEMLPQEDQEHWDITQKAQGGGERDFDWNLRNLRPERYNKSK							
BFIV*12	EL-T---IQ-A-----Q-W--T-----GEL-VH-N-TA-RYV-RT-WIAAKA-QY--G---IG--N-QIDRE--GI-QR---QTG							
<i>a2 domain</i>	90.	100.	110.	120.	130.	140.	150.	160.
YFV <sub>w</sub> *7	GSHTMQMMFGCDILEDGSIQGYDQAFDGRDFLAFDMDTMTFTAADPVAEITKRRWETEGTYAERWKHELGTVCVQNLRRLRLEHGKAALKRR							
BFIV*12	---V-W-Y-----G-P-----Y-M-Y-----T---KG-----V-E-VP---K--E-SE/P-----NY-EET--EW---V-Y---E-G--							
<i>a3 domain</i>	180.	190.	200.	210.	220.	230.	240.	250.
YFV <sub>w</sub> *7	VQPEVRVWGKEADGILTLSCAHGFYPRITISWMKDGWVRDQETRWGGIVPNSDGTTHASAAIDVLBEDGDKYWCVRVEHASLPQGLFSW							
BFIV*12	ER-----R-----VV-L---A--G-DAHS-----G-----TWVT--AQ-G-----Q-----Y--							
<i>Transmembrane domain</i>	280.	290.	300.					
YFV <sub>w</sub> *7	EP/QPNLPIVAGAVVAIVAV/IAAVVGLVVMKSKS							
BFIV*12	--P---V-----VA-----IA-MVG--FIYRRHA							
<i>Cytoplasmic domains</i>	310.	320.	330.					
	GKEKKGYEAAAGHDGESSGSGATGSEPSI							
	--KG---NI-PDRE-G--S-S---N-A-							

Figure 4

GGTGTGGATTTCATCATCTACAGACGCCACGCAGGTAAAAGCAGAGGGGTGCAGGCGGGCAGTGGTGGCAGTGGGGGGATCTG  
GGTCCCCCTTGGGAGCCCTCAGCCTGGCTGTGATGTGAACCTGTGTTGATTTCATCTCTCTGTCTGCAGGGGAAGAAGGGGAAGG  
GCTACAACATCGCGCCCGGTGAGTGATGAGGGCAGCGCTGTCCCCACCTCTGCCCAGTGCCAGGGCGGTCTCTGGGTCTGCA  
CTTTCTCCCAGGGTACCCATTCTGCTTGGGGCTGCTCCACGCCCCATAGGGAGCACAGGGCTGGGTCTCACAGCTGTTC  
CTCCCTTATAGACAGGGAAGGTGGATCCAGCAGCTCGAGCACAGGTGCGGTGTGGGGCTGTGGGTGGGAGGGGTCCGTGTGC  
TCTCTGTGGTACTGCCAGGGCTGGGCTATGCTGGGGCTCTGCGGGGAGACCCCGGAGCAGAGGGTTGGGATGTGAACATGG  
GCCCCGTGGGACACCATCTCTTCTCATCCCCACAGGGAGCAACCCCTCCATCTGAGTGCTGTGCTTCAGCATGCACGAAGCCA  
ACAGTCCACACCAGCATTTGGGGTCAGTGATGGGCACAGCCCCATCCTCTTGACCTCTCACATCTCGTTCTGCTTCCTATGCT  
GACTGTTATGC

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Figure 5

GGGGAGAAAGCGGGAGCTGCAGGTGGGGCCTGGACCCCCTTGGGAATGCCCATGTTCTGACATGAGCTTAATGTTACACTTC  
TTTCTATCTGTAGGGAAGGAGAAGAAGGGTTATGAAGCAGCGCCAGGTGAGTGCCAAGGGCAGCGCTTTACCCTGCCAGTGCT  
TGGGGTCAGGGCACTCTGGGGCCCCCTCGTTGCTTTTGGGGTCACAGTGCAGGTGGTGGCATGATGCTCCATGCCCCACAGCGA  
GCACAGAGCCAGGGCTCATGGCTCTCCCTCCCTTGCAAGGCCAGGGCGGAGAATCCAGCATATCGGCCACAGGTATAgTGTGGA  
ATGGGGGTTTCAGGAGGGGTCCCTGTGTTGGAGCATTTCCCAgTCCCTGCACTCCCCTGTTGGACCCACGGCCGGGGCAATAC  
TGGGCCcAaCCCTCCCTGGAGAAcCCCCAGGGTGGTGAGTCGGGACGGGGACGTGGTCCCATATGACACCACCTCTTCTCACC  
CGCACAGGAAGTGAACCTCCCTTCTGAGTGCTGTGTTACTTCAGCCAGCCCCTGCATGCATGTGTTTGGAGTGTGTGGGTGTGT  
GTATCTCAGTGTGTGCTCAACTTCCTGCATCTCCTCGGGCTGACA

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**A.**

Dam A186	<u>A186 family</u>												Sire 186	<u>B186 family</u>												Dam B186		
Y3---																									Kb			
B11----																									~4.1			
BR9-																									~2.3			
B11----																									~2.1			
																									~1.9			
BR9-																												
Y3---																												
B11----																												
BR9-																									~0.6			
BR9-																												
-B11----																												
	Y1/2	Y1/1	Y1/2	Y1/1	Y1/1	Y1/2	Y1/2	Y1/1	Y1/2	Y1/2	Y2/2	Y2/2	Y1/2	Y1/2	Y2/2	Y2/2	Y1/2	Y1/2	Y2/3	Y1/2	Y1/3	Y1/3	Y1/1	Y1/3	Y2/3	Y1/2	Y2/3	Y1/3

**B.**

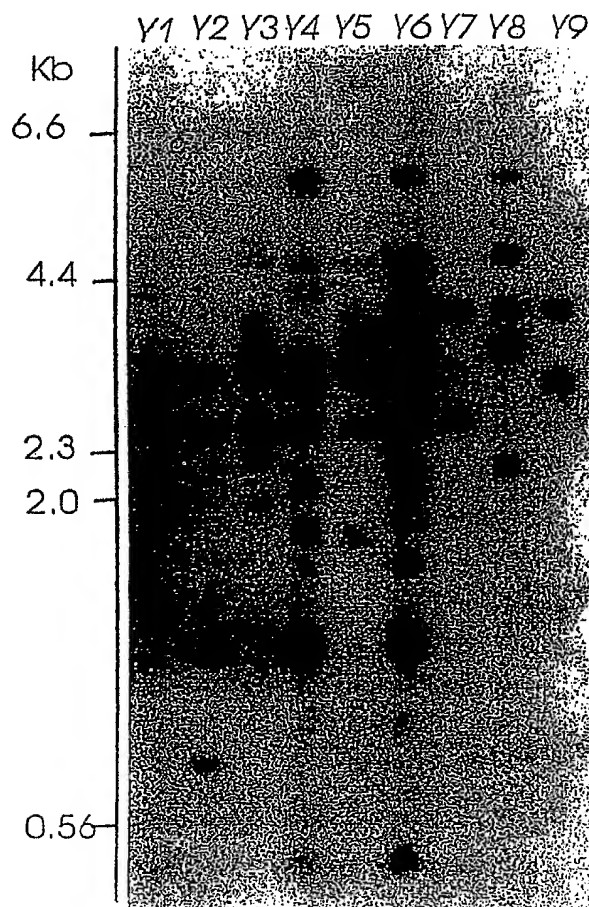
Y2-																											
Y1 or Y2 or Y3 ----																									~50		
Y3--Y2-																									~4.1		
Y2-																											
Y3-----																											
Y1 or Y3----																									~0.6		
Y2-																											
	BR9/11	BR9/11	BR9/11	BR9/11	BR9/11	B11/11	BR9/9	BR9/9	B11/11	BR9/11	BR9/11	BR9/9	BR9/11	BR9/11	BR9/9	BR9/11	BR9/11	BR9/11	B11/11	BR9/9	BR9/11	BR9/11	BR9/11	BR9/9	BR9/11	B11/11	BR9/11

**C.**

B11----																									~2.3
BR9-																									~2.1
B11----																									~1.9

Figure 7



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Figure 8

